

```

# from Ito and Houston (2004)
calc_Hepatic_Clearance <- function(Params,model="well-stirred",Dn=0.17)
{
  CLint <- get_param("CLint",Params,"calc_Hepatic_Clearance")
  fub <- get_param("fub",Params,"calc_Hepatic_Clearance")
  BW <- get_param("BW",Params,"calc_Hepatic_Clearance")
  Qh <- get_param("Qhc",Params,"calc_Hepatic_Clearance")*BW
  liver.volume.per.kgBW <- get_param("liver.volume.per.kgBW",Params,"calc_Hepatic_Clearance")
  tissue.density <- get_param("tissue.density",Params,"calc_Hepatic_Clearance")

  if (!(model %in% c("well-stirred","parallel tube","dispersion")))
    stop("Model other than \"well-stirred,\" \"parallel tube,\" or \"dispersion\" specified.")

  # Convert from mL/min/10^6 cells to mL/min/g liver
  CLint <- CLint*cells.per.g.liver
  # Convert from mL/min/g liver to uL/min
  CLint <- CLint*liver.volume.per.kgBW*1000*tissue.density*BW

  if (model == "well-stirred")
    CLh <- Qh*fub*CLint/(Qh+fub*CLint)
  else if (model == "parallel tube")
    CLh <- Qh*(1-exp(-fub*CLint/Qh))
  else if (model == "dispersion")
  {
    Rn <- fub*CLint/Qh
    a <- sqrt(1 + 4*Rn*Dn)
    CLh <- Qh*(1 - 4*a/((1+a)^2*exp((a-1)/2/Dn)-(1-a)^2*exp(-(a+1)/2/Dn)))
  }

  return(CLh)
}

```